

APPROVED	O.G. FIG.	CLASS/SUBCLASS
	BY	
DRAFTSMAN		

VH DOMAIN

	10	20	30	40
MaE11	DVQLQESGPG * * *	LVKPSQSLSL * * *	ACSVTGYSITS * * *	[GYSWN]WIRQF *
F(ab)-2	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSITS * ****	[GYSWN]WIRQA * **** *
humIII	EVQLVESGGG	LVQPGGSLRL	SCAASGFTF-S	[DYAMS]WVRQA
	49	60	70	80
MaE11	PGNKLEWMG * * *	[SITYDGSSNYN PSLKN]RISVT * * * * *		RDTSQNQFFL * * * *
F(ab)-2	PGKGLEWVA	[SITYDGSTNYA DSVKG]RFTIS * * * * *		RDDSKNTFYL
humIII	PGKGLEWVA	[VISNGSDTYA DSVKG]RFTIS		RDDSKNTLYL
	82abc 90	100abcd 103	113	
MaE11	KLNSATAEDTATY * * *	YCAR[GSHYFGHWHFAV] * *	WGAGTTVT	VSS
F(ab)-2	QMNSLRAEDTAVY	YCAR[GSHYFGHWHFAV] * * * * *	WGQGTlVT	VSS
humIII	QMNSLRAEDTAVY	YCAR[DSRFF-----DV]	WGQGTlVT	VSS

VL DOMAIN

	10	20	30 32abcd	40
MaE11	DIQLTQSPAS *	LAVSLGQRAT * * * *	ISC[KASQSVD YDGDSYMN]WYQQKP * *	
F(ab)-2	DIQLTQSPSS	LSASVGDRVT	ITC[RASQSVD YDGDSYMN]WYQQKP **** *	
humk1	DIQMTQSPSS	LSASVGDRVT	ITC[RASQSVD IS--SYLN]WYQQKP	
	49	60	70	80
MaE11	GQPPILLIY * * *	[AASYLGS]EIPA * * *	RFSGSGSGTD	FTLNHPVEE * * * * *
F(ab)-2	GKAPKLLIY	[AASYLES]GVPS *	RFSGSGSGTD	FTLTISLQP
humkI	GKAPKLLIY	[AASSLES]GVPS	RFSGSGSGTD	FTLTISLQP
	88	97	107	
MaE11	EDAATFYC * *	[QQSHEDPYT]	FGAGTKLEIK * *	
F(ab)-2	EDFATYYC	[QQSHEDPYT] ****	FGQGTKVEIK	
humk1	EDFATYYC	[QQYNSLPYT]	FGQGTKVEIK	

FIG._1

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LIGHT CHAIN

	10	20	30	40
e27	DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY
e26	DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY
e426	DIQLTQSPSS	LSASVGDRVT	ITCRASQSV	YEGDSYLNWY
e25	DIQLTQSPSS	LSASVGDRVT	ITCRASQSV	YDGD SYMNWY

CDR-L1

	50	60	70	80
e27	QKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
e26	QKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
e426	QKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS
e25	QKPGKAPKL	LIYAASYLES	GVPSRFSGSG	SGTDFTLTIS

CDR-L2

	90	100	110	
e27	SLQPEDFATY	YCQOSHEDPY	TFGQGTKVEI	KRTV
e26	SLQPEDFATY	YCQOSHEDPY	TFGQGTKVEI	KRTV
e426	SLQPEDFATY	YCQOSHEDPY	TFGQGTKVEI	KRTV
e25	SLQPEDFATY	YCQOSHEDPY	TFGQGTKVEI	KRTV

CDR-L3

HEAVY CHAIN

	10	20	30	40
e27	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
e26	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
e426	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ
e25	EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ

CDR-H1

	50	60	70	80
e27	APGKGLEWVA	SIKYSGETKY	NPSVKGRITI	SRDDSKNTFY
e26	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI	SRDDSKNTFY
e426	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI	SRDDSKNTFY
e25	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI	SRDDSKNTFY

CDR-H2

	90	100	110	
e27	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
e26	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
e426	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG
e25	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQG

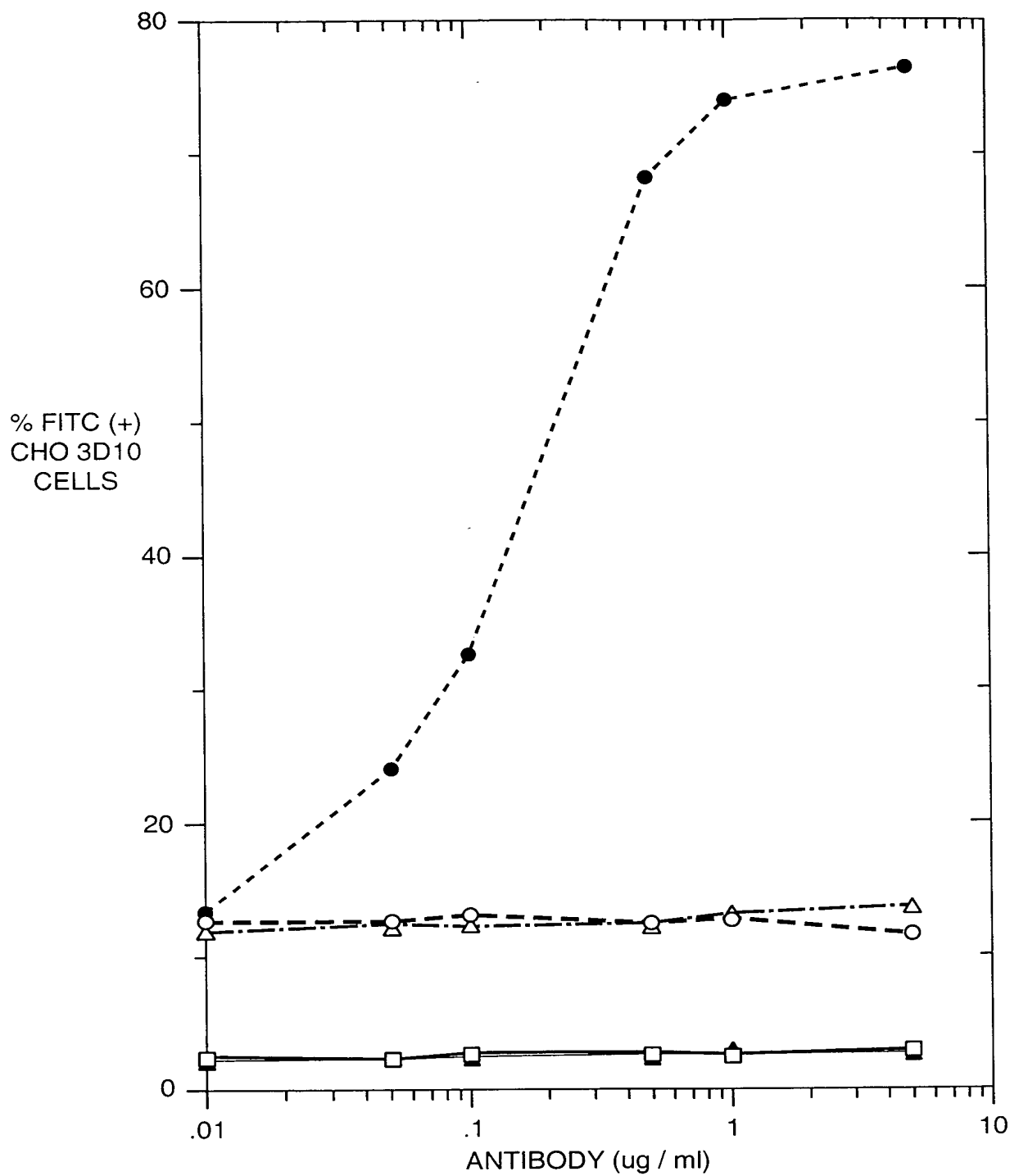
CDR-H3

FIG._2

[illegible]

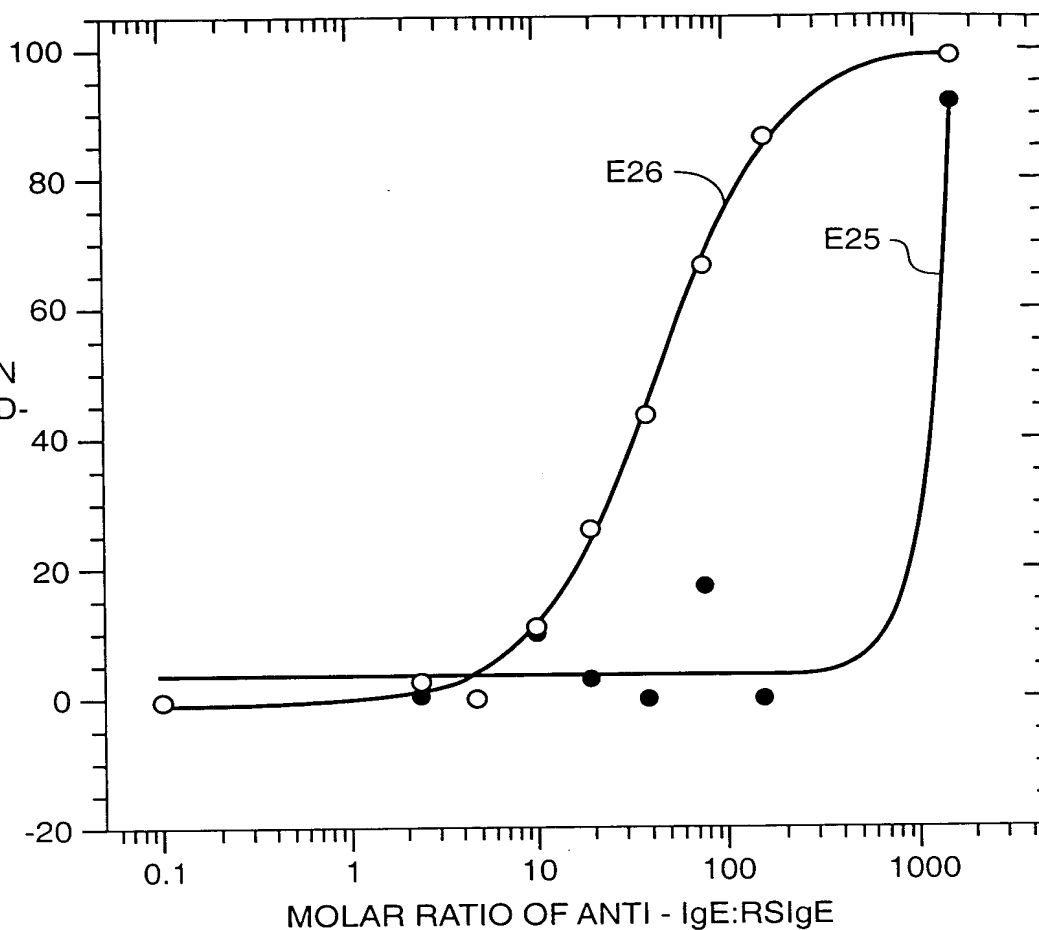
FIG._3

APPROVED	Q. G. FIG.
BY	CLASS/SUBCL/SS
DRAFTSMAN	

**FIG. 4**

APPROVED	Q.G. FIG.
BY	CLASS/SUBCL/SS
DRAFTSMAN	

% INHIBITION
OF RAGWEED-
INDUCED
HISTAMINE
RELEASE



$$y = ((m1 - m4) / (1 + (m0 / m3)^{m2})) \dots$$

	VALUE	ERROR
m1	3.7289	3.2575
m2	3.2312	2044.6
m3	3421.3	7.095e+07
m4	1226.5	7.4139e+07
Chisq	293.26	NA
R	0.97929	NA

$$y = ((m1 - m4) / (1 + (m0 / m3)^{m2})) \dots$$

	VALUE	ERROR
m1	-0.78645	1.7681
m2	1.3544	0.11267
m3	44.486	3.1931
m4	100.07	2.6239
Chisq	31.442	NA
R	0.99867	NA

FIG. 5

APPROVED	J.G. FIG.	CLASS/SUBCLASS
BY		
DRAFTSMAN		

Gene	Exons	Introns
G1	1	0
G2	1	0
G3	1	0
G4	1	0
G5	1	0
G6	1	0
G7	1	0
G8	1	0
G9	1	0
G10	1	0
G11	1	0
G12	1	0

Bar chart showing the number of E/E genotypes for different e426 LIBRARY categories (a, b, c, d'). The y-axis represents the count from 0 to 12. The legend identifies six E/E genotypes: (1) solid black, (2) dotted, (3) diagonal lines, (4) white, (5) horizontal lines, and (6) vertical lines.

e426 LIBRARY	E / E (1)	E / E (2)	E / E (3)	E / E (4)	E / E (5)	E / E (6)
a	0	0.4	0.4	2.5	6.4	5.5
b	0	1.1	3.1	3.3	11.5	6.7
c	0	0.2	0.2	1.4	2.6	0.9
d'	0	0	0	3.1	0	0.6

FIG. 6

+

APPROVED	O.G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	38.5	12.5	25	65	0.1	3.2	0.95
Gender	1.2	0.4	1	2	0.2	3.5	0.98
Marital Status	1.5	0.5	1	3	0.3	3.8	0.97
Education	12.5	2.5	9	16	0.4	4.1	0.96
Income	1500	500	1000	2500	0.5	4.5	0.94
Occupation	1.8	0.6	1	3	0.6	4.8	0.93
Health Status	2.5	0.8	1	4	0.7	5.1	0.92
Stress Level	3.5	1.2	2	5	0.8	5.5	0.91
Life Satisfaction	4.0	1.0	3	5	0.9	5.8	0.90
Resilience	3.8	1.1	2	5	0.8	5.6	0.91
Emotional Stability	3.2	0.9	2	4	0.7	5.3	0.92
Social Support	3.0	0.8	2	4	0.6	5.2	0.93
Life Events	2.8	0.7	2	4	0.5	5.0	0.94
Personal Growth	3.5	1.0	2	5	0.7	5.4	0.92
Life Satisfaction	4.0	1.0	3	5	0.9	5.8	0.90
Resilience	3.8	1.1	2	5	0.8	5.6	0.91
Emotional Stability	3.2	0.9	2	4	0.7	5.3	0.92
Social Support	3.0	0.8	2	4	0.6	5.2	0.93
Life Events	2.8	0.7	2	4	0.5	5.0	0.94
Personal Growth	3.5	1.0	2	5	0.7	5.4	0.92

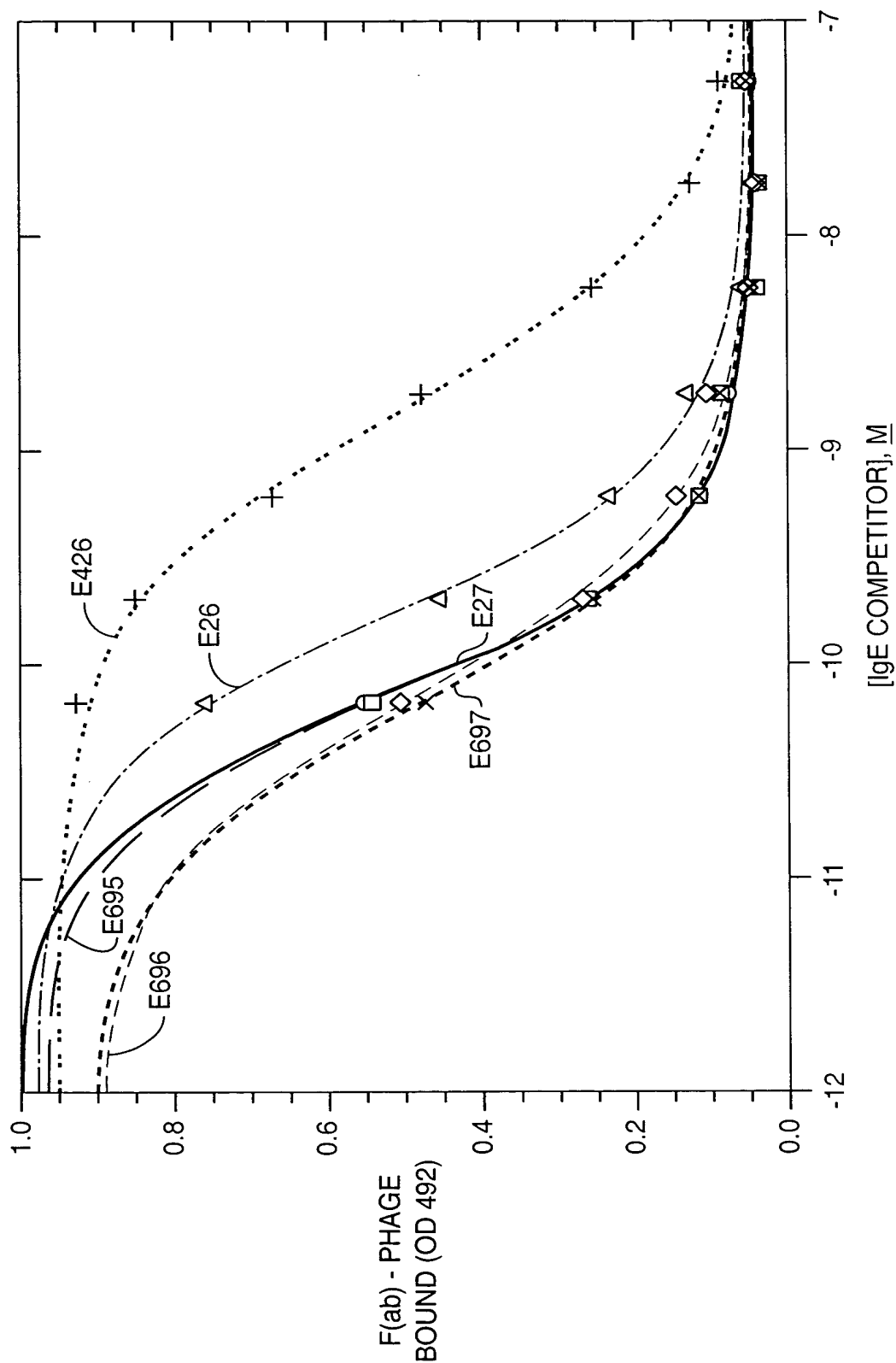
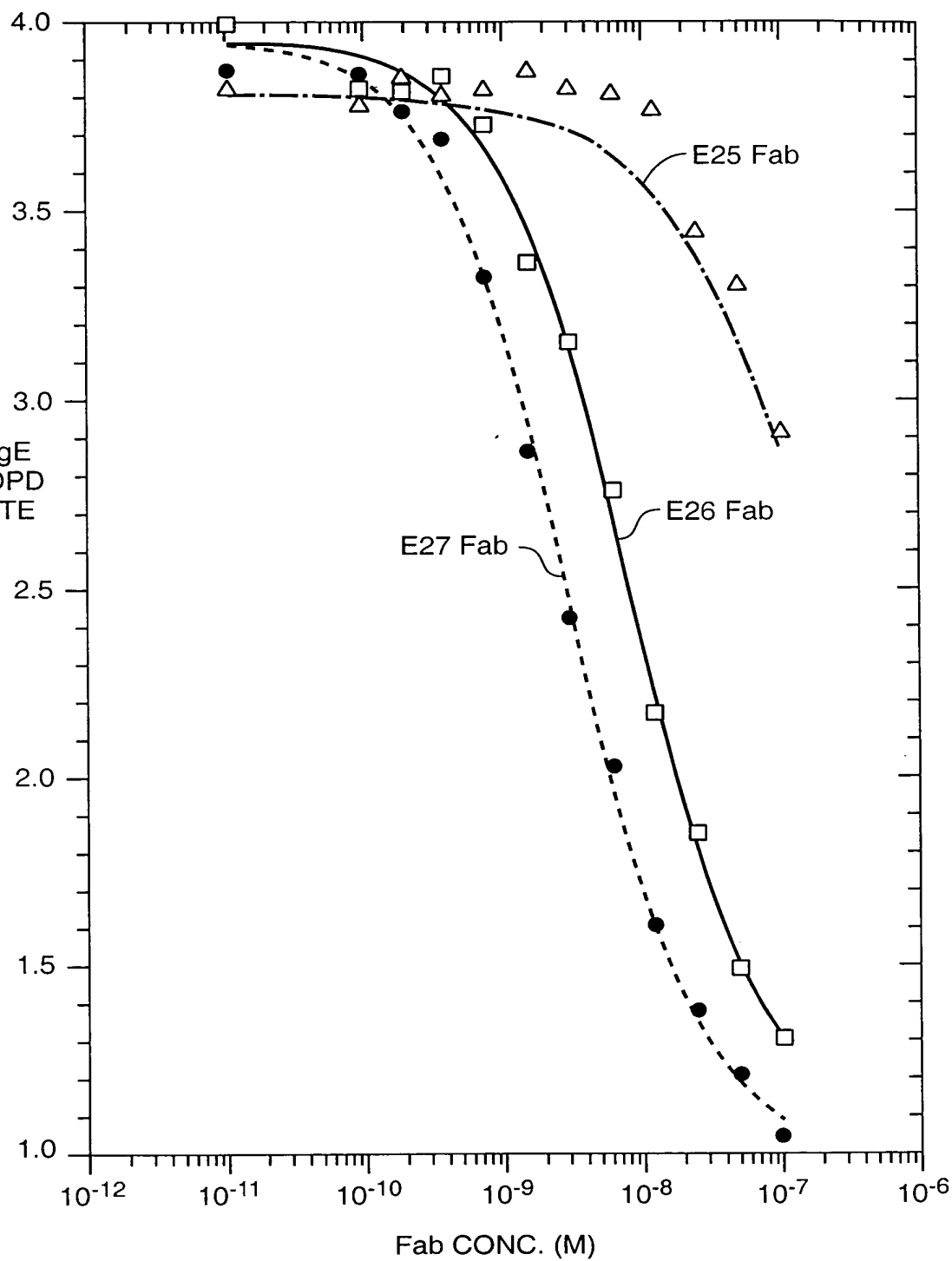


FIG.-7

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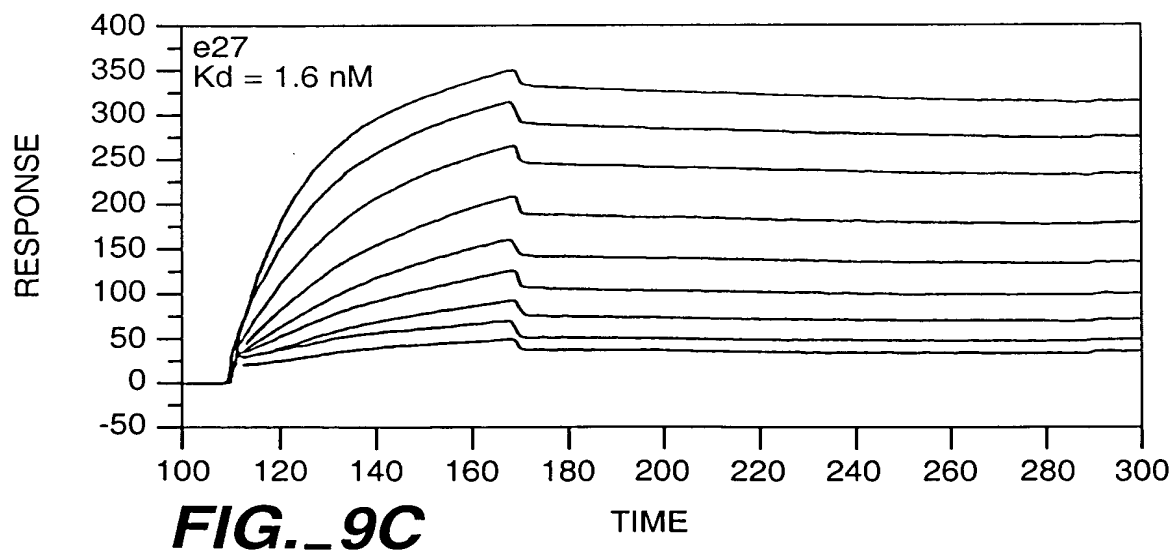
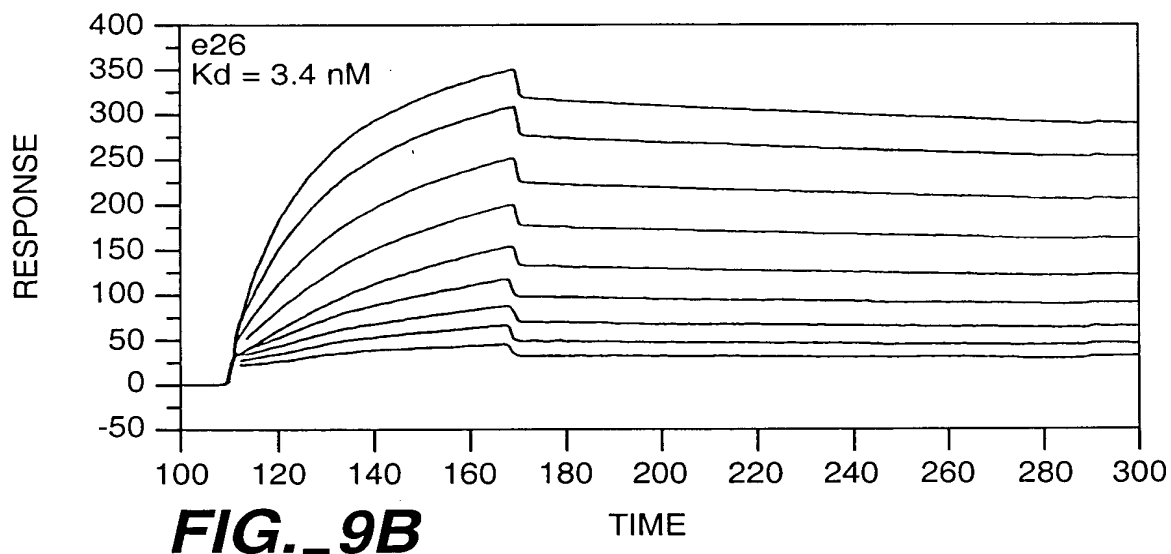
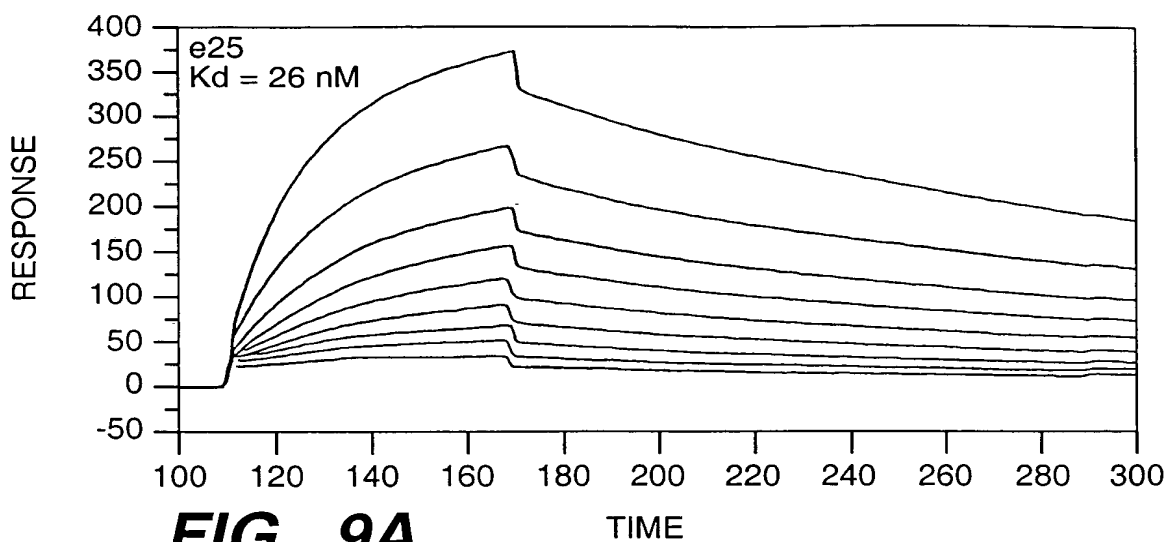
APPROVED	Q. G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

BIOTIN - IgE
BINDING OPD
SUBSTRATE
490 nm

**FIG. 8**

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APPROVED	C.G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	



APPROVED	O. G. FIG.
BY	CLASS SUBCL/SS
DRAFTSMAN	

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1 GAATTCAACT TCTCCATACT TTGGATAAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTATTT AAGCTTGCCC AAAAAAGA AGATCGAAT
 CTTAAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCGT TACTTTTGTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
 CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTGCG CAACTAATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTACGTA
 CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA CTTGTCTATAA AGTTGTCCAG GCGGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTTGTAACATA GAATTCGAGC
 TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATA AAAATTACAT AAACATTGAT CTTAAGCTCG

401 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAAT ATCGCATTTC TTCTTGCTATC TATGTTTCGTT TTTTCTATTG CTACAAACGC
 AGCCATGGC CCCTAGGAGA GCTCCAACTC CACTAAAATA CTTTCTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC GATGTTTGCG

501 GTACGCTGAT ATCCAGCTGA CCCAGTCCC GAGCTCCCTG TCCGCTCTG TGGCGGATAG GGTCAACCATC ACCTGCCGTG CCAGTCAGAG CGTCGATTAC
 CATGCGACTA TAGGTCGACT GGGTCAGGG CTCGAGGGAC AGCGGAGAC ACCCGCTATC CCAGTGGTAG TGGACGGCAC GGTCAGTCTC GCAGCTAATG

1 Alaasp IleGlnLeuF hrGlnSerPr oSerSerLeu SerAlaSerV alGlyAspAr gValThrIle ThrCysArgA laSerGlnSe rValAspTyr
 Begin light chain

601 GAAGGTGATA GCTACCTGAA CTGGTATCAA CAGAAACCAG GAAAAGCTCC GAAACTACTG ATTTACGCGG CCTCGTACCT GGAGTCTGGA GTCCCTTCTC
 CTTCCACTAT CGATGGACTT GACCATAGTT GTCTTTGGTC CTTTTCGAGG CTTTGATGAC TAAATGCGCC GGAGCATGGA CCTCAGACCT CAGGGAAGAG

33 GluGlyAspS erTyrLeuAs nTrpTyrGln GlnLysProG lylsAlaPr oLysLeuLeu IleTyrAlaa laSerTyrLe uGluSerGly ValProSerArg

701 GCTTCTCTGG ATCCGGTTCT GGGACGGATT TCACTCTGAC CATCAGCAGT CTGCAGCCAG AAGACTTTCG AACTTATTAC TGTACGCAAA GTCACGAGGA
 CGAAGAGACC TAGGCCAAGA CCTGCGCTAA AGTGAGACTG GTAGTCGTCA GACGTCGGTC TTCTGAGCGG TTGAATAATG ACAGTCGTTT CAGTGTCTCT

67 PheSerG1 ySerGlySer GlyThrAspP heThrLeuTh rIleSerSer LeuGlnProG luAspPheAl aThrTyrTyr CysGlnGlnS erHisGluAsp

801 TCCGTPACACA TTTGGACAGG GTACCAAGGT GGAGATCAAA CGAAGTGTGG CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT
 AGGCATGTGT AAACCTGTCC CATGTTCCA CTTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGCGGTA GACTACTCGT CAACCTTAGA

100 ProTyrThr PheGlyGlnG lyThrLysVa lGluIleLys ArgThrVala laAlaProse rValPheIle PheProProS erAspGluGl nLeuLysSer

901 GGAACCTGCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGTGGG ATAACGCCCT CCAATCGGGT AACTCCCAGG
 CCTTGACGAA GACAACACAC GGACGACTTA TTGAAGATAG GGTCCTCCG GTTTCATGTC ACCTTCACC TATTGCGGGA GGTAGCCCA TTGAGGGTCC

133 GlyThrAlaS erValValCy sLeuLeuAsn AsnPheTyrP roArgGluAl aLysValGln TrpLysVala spAsnAlaLe uGlnSerGly AsnSerGlnGlu

FIG.- 10A

APPROVED	O. G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

1001 AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG
TCTCACAGTG TCTCGTCTG TCGTTCTCTG TCGGATGTC GGAGTCGTCG TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGGGAC
167 SerValTh rGluGlnAsp SerLysAspS erThrTySe rLeuSerSer ThrLeuThrL euSerLysAl aAspTyGlu LyHisLysV alTyAlaCys

1101 CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TTAAGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT
GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC AATTCGACTA GGAGATGCGG CCTGCGTAGC ACCGGGATCA
200 GluValThr HisGlnGlyL euSerSerPr oValThrLys SerPheAsnA rGlyGluCy SOC*
end light chain

1201 ACGCAAGTTC ACGTAAAAAG GGTATCTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA
TGC GTTCAAG TGCATTTTC CCATAGATCT CCAACTCCAC TAAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT

1301 CAAACGCGTA CGCTGAGGT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCTGT GCAGTTTCTG GCTACTCCAT
GTTTGGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCAAAGAC CGATGAGGTA
1 GluVal GlnLeuValG luSerGlyG lGlyLeuVal GlnProGlyG lySerLeuAr gLeuSerCys AlaValSerG lyTySerIle
Begin heavy chain

1401 CACCTCCGGA TACAGCTGGA ACTGGATCCG TCAGGCCCGG GGTAAAGGGC TGGATGGGT TGCATCGATT ACGTATGACG GATCGACTAA CTATAACCCCT
GTGGAGGCC ATGTCGACCT TGACCTAGG AGTCCGGGG CCATTCCCGG ACCTTACCCA ACGTAGCTAA TGCACTACTGC CTAGCTGATT GATATTGGGA
30 ThrSerGly TyrSerTrpA snTrpIleAr gGlnAlaPro GlyLysGlyL euGluTrpVa lAlaSerIle ThrTyAspG lySerThrAs nTyAsnPro

1501 AGCGTCAAG GCCGTATCAC TATAAGTCGC GACGATTCCA AAAACACATT CTACCTGCAG ATGAACAGCC TGGTGTCTGA GGACACTGCC GTCTATTATT
TCGCAGTTCC CGGCATAGTG ATATTACGG CTGCTAAGGT TTTTGTGTA GATGGACGTC TACTTGTCCG ACGCACGACT CCTGTGACGG CAGATAATAA
63 SerValLysG lyArgIleTh rIleSerArg AspAspSerL ysAsnThrPh eTyLeuGln MetAsnSerL euArgAlaGl uAspThrAla ValTyTyCys

1601 GTGCTCGAG CAGCCACTAT TTCGGTCACT GGCACTTCGC CGTGTGGGT CAAGGAACCC TGGTCACCGT CTCCTCGGCC TCCACCAAGG GCCCATCGGT
CAGGACTCC GTCGGTGATA AAGCCAGTGA CCGTGAAGCG GCACACCCCA GTTCTTGGG ACCAGTGGCA GAGGAGCCGG AGGTGTTCC CGGCTAGCCA
97 AlaArgG l ySerHisTy rPheGlyHis rPheGlyHis aValTrpGly GlnGlyThrL euValThrVa lSerSerAla SerThrLysG lyProSerVal

1701 CTTCCCCCTA GCACCTCCT CCAAGAGCAC CTCTGGGGG ACAGCGGGCC TGGGTGCTT GGTCAAGGAC TACTTCCCC AACCGGTGAC GGTGTCTGG
GAAGGGGGAT CGTGGAGGA GGTCTCTGTG GAGACCCCGG TGTCGGCGGG ACCGACGGA CCAGTTCTCTG ATGAAGGGG TTGGCCACTG CCACAGCACC
130 PheProLeu AlaProSerS erLysSerTh rSerGlyGly ThrAlaAlaL euGlyCysLe uValLysAsp TyrPheProG luProValTh rValSerTrp

1801 AACTCAGGCG CCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCTTACA GTCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA
TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGAAGGGCC GACAGGATGT CAGAGTCTT GAGATGAGG AGTCGTCGCA CCACTGGCAC GGGAGTCTGT
163 AsnSerGlyA laLeuThrSe rGlyValHis ThrPheProA laValLeuG l nSerSerGly LeuTySerL euSerSerVa lValThrVal ProSerSerSer

FIG. 10B

APPROVED	O. G. FIG.
BY	CLASS SUBCL/SS
DRAFTSMAN	

1901 GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA AAACACACAC
CGAACCCGCG GGTCTGGATG TAGACGTGCG ACTTAGTGTT CGGGTCGTGG TGGTTCACAC TGTCTTTTCA ACTCGGGTTT AGAACACTGT TTGAGTGTG
197 LeuGlyTh rGlnThrTyr IleCysAsnV alaAsnHisLy sProSerAsn ThrLysValA sPlyLysVa lGluProLys SerCysAspL yThrHisThr
end of heavy chain

2001 CTAGAGTGGC GGTGGCTCTG GTTCCGGTGA TTTTGATTAT GAAAAGATGG CAAACGCTAA TAAGGGGGCT ATGACCGAAA ATGCCGATGA AAACGGCGTA
GATCTCACCG CCACCGAGAC CAAGGCCACT AAAACTAATA CTTTCTTACC GTTTGCGATT ATTCCCCCGA TACTGGCTTT TACGGCTACT TTGCGCGAT
230 AM*SerGly GlyGlySerG lySerGlyAs pPheAspTyr GlulysMeta laasnAlaAs nLysGlyAla MetThrGluA snAlaAspG1 uasnAlaLeu
fusion to g3p C-terminal domain

2101 CAGCTGACG CTAAAGGCAA ACTTGATCT GTGCTACTG ATTACGGTGC TGCTATCGAT GGTTCATTG GTGACGTTTC CGGCCTTGCT AATGGTAATG
GTCAGACTGC GATTTCGTT TGAACTAAGA CAGCGATGAC TAATGCCACG ACATAGCTA CCAAGTAAC CACTGCAAAG GCCGGAACGA TTACCATTTAC
263 GlnSerAspA laLysGlyLy sLeuAspSer ValAlaThrA sPtyrGlyAl aalaIleAsp GlyPheIleG lyAspValSe rGlyLeuAla AsnGlyAsnGly

2201 GTGCTACTGG TGATTTTGCT GGCTCTAATT CCCAAATGGC TCAAGTCGGT GACGGTGATA ATTCACCTTT AATGAATAAT TTCCGTCAAT ATTTACCTTC
CAGCATGACC ACTAAAACGA CCGAGATTAA GGGTTTACCG AGTTCAGCCA CTGCCACTAT TAAGTGGAAA TTACTTATTA AAGGCAGTTA TAAATGGAAG
297 AlaThrG1 yAspPheAla GlySerAsnS erGlnMetal aGlnValGly AspGlyAspA snSerProLe uMetAsnAsn PheArgGlnT yrLeuProSer

2301 CCTCCCTCAA TCGGTTGAAT GTCGCCCTTT TGTCTTTAGC GCTGGTAAAC CATATGAATT TTCTATTGAT TGTGACAAAA TAAACTTATT CCTGGGTGTC
GGAGGGAGTT AGCCAACTTA CAGCGGGAAA ACAGAAATCG CGACCATTTG GTATACCTAA AAGATACTA ACACTGTTTT ATTTGAATAA GGCACCACAG
330 LeuProGln SerValGluC ysArgProPh eValPheSer AlaGlyLysP roTyrGluPh eSerIleasp CysAspLysI leasnLeuPh eArgGlyVal

2401 TTTGCGTTTC TTTTATATGT TGCCACCTTT ATGTATGTAT TTTCTACGTT TGCTAACATA CTGCGTAATA AGGAGTCTTA ATCATGCCAG TTCTTTTGGC
AAACGCAAAG AAAATATACA ACGGTGGA AAGATGCAA ACGATTGTAT GACGCATTAT TCCTCAGAAAT TAGTACGGTC AAGAAAAACCG
363 PheAlaPheL euLeuTyrVa lAlaThrPhe MetTyrValP heSerThrPh eAlaAsnIle LeuArgAsnL ysGluSerOC *
end of g3p domain

2501 TAGCGCCGCC CTATACCTTG TCTGCCCTCC CGCGTTGCGT CGCGGTGCGT GGAGCCGGGC CACCTCGACC TGAATGGAAG CCGCGGGCAC CTCGCTAACG
ATCGCGGCGG GATATGGAAC AGACGGAGG GCGCAACGCA CGCGCCCGTA CCTCGGCCCG GTGGAGCTGG ACTTACCTTC GGCCGCCGCGT GAGCGATTGC

2601 GATTCAACCAC TCCAAGAATT GGAGCCAATC AATTCTTGG GAGAACTGTG AATGCGCAAA CCAACCCCTTG GCAGAACATA TCCATCGCGT CCGCCATCTC
CTAAGTGGTG AGGTTCTTAA CCTCGGTTAG TTAAGAACGC CTCTTGACAC TTACGCGTTT GGTGGGAAC CGTCTGTAT AGGTAGCGCA GCGCGTAGAG

2701 CAGCAGCCGC ACGCGGCGCA TCTCGGGGCG GGTGGGTCC TGGCCACGGG TGCGCATGAT CGTGCTCCTG TCCTTGAGGA CCCGGCTAGG CTGGCGGGGT
GTCGTGCGCG TCGCGCGCGT AGAGCCCGTC GCAACCCAGG ACCGGTGCCC ACGGTACTA GCACGAGGAC AGCAACTCCT GGGCCGATCC GACCGCCCCA

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FIG. 10C

APPROVED	O. G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

[illegible]

22801	TGCCTTACTG GTTAGCAGAA TGAATCACCG ATACGGGAGC GAACGTGAAG CGACTGCTGC TGCAAAACGT CTGCACCTG AGCAACAACA TGAATGGTCT	ACGGAATGAC CAATCGTCTT ACTTAGTGGC TATGCGCTCG CTTGCACTTC GCTGACGACG ACGTTTTGCA GACGCTGGAC TCGTTGTGTG ACTTACCAGA
22901	TCGGTTTCCG TGTTTCGTAA AGTCTGGAAA CGCGGAAGTC AGCGCCCTGC ACCATTATGT TCCGGATCTG CATCGCAGGA TGCTGCTGGC TACCCTGTGG	AGCCAAAGGC ACAAAGCAAT TCAGACCTTT GCGCCTTCAG TCGCGGGACG TGGTAATACA AGGCCTAGAC GTAGCGTCTT ACGACGACCG ATGGGACACC
33001	AACACCTACA TCTGTATTAA CGAAGCGCTG GCATTGACCC TGAGTGATTT TTCTCTGGTC CCGCCGCATC CATACCGCA GTTGTTTACC CTCACAACGT	TTGTGGATGT AGACATAATT GCTTCGCGAC CGTAACGGG ACTCACTAAA AAGAGACCAG GCGGGCGTAG GTATGGCGGT CAACAAATGG GAGTGTGCA
33101	TCCAGTAACC GGGCATGTTT ATCATCAGTA ACCCGTATCG ACCGTTGATC TGAGCATCCT TGAGTGGCC GCCTTTATCAG ATCGGTATCA TTACCCCCAT TCCCCCTTAC	AGGTCAATGG CCCGTACAAG TAGTAGTCAT TGGGCATAGC ACTCGTAGGA GAGAGCAAAG TAGCCATAGT AATGGGGTA CTGTCTTTA AGGGGAATG
33201	ACGGAGGCAT CAAGTGACCA AACAGGAAA AACCGCCCTT AACATGGCC GCCTTTATCAG AAGCCAGACA TTAACGCTTC TGGAGAAACT CAACGAGCTG	TGCCTCCGTA GTTCACTGGT TTGTCTCTTT TTGGCGGGAA TTGTACCGGG CGAATAGTC TTCGGTCTGT AATTGCGAAG ACCTCTTTGA GTTGTCTGAC
33301	GACGCGGATG AACAGGCAGA CATCTGTGAA TCGCTTCACG ACCACGCTGA ACCAGGATCC CGAATTGTA ACGTTAATA TTTTGTTTAA	CTGCGCCTAC TTGTCCGTCT GTAGACACTT AGCGAAGTGC TGGTGGACT ACTCGAAATG GCGTCTTAGG CCTTTAACAT TTGCAATTAT AAAACAATTT
33401	ATTGCGGTTA AATTTTGTGT AAATCAGCTC AATTTTTAAC CATATAGCCG AAATCGGCAA AATCCCTTAT AATAGACCGA AATAGGTTG	TAAGCGCAAT TTAAAAACAA TTTAGTTCGAG TAAAAAATG GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC TTATCTGGCT CTATCCCAAC
33501	AGTGTGTGTC CAGTTTGGAA CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAA CCGTCTATCA GGGCTATGG CCATACGCTG	TCACAACAAG GTCAAACCTT GTTCTCAGGT GATAATTCTT TGCACCTGAG GTTGCAGTTT CCCGCTTTTT GGCAGATAGT CCCGATACCG GGTGATGAC
33601	AACCATCACC CTAATCAAGT TTTTGTGGGT CGAGGTGCGG TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCTGATT AGAGCTTGAC GGGGAAAGCC	TTGGTAGTGG GATTAGTTCA AAAAACCCCA GCTCCACGGC ATTTCTGTAT TTAGCCCTGG GATTTCCCTC GGGGGCTAAA TCTCGAACTG CCCCTTTCCG
33701	GGCGAACGTG GCGAGAAAGG AAGGGAAGAA AGCGAAAGGA GCGGGCGCTA GCGGGCGCTA TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCTGATT AGAGCTTGAC	CCGCTTGAC CGCTCTTTCC TTCCCTTCTT TCGCTTTCTT GCTCCACGGC GTTATCCGCT TTAGCCCTGG GATTTCCCTC GGGGGCTAAA TCTCGAACTG
33801	GCGCTTAATG CGCGGCTACA GGGCGCGTCC GGATCTCTGC GATCTCTGCC GGTGATGAC CCGTGTGATC TCTGACACAT GCAGCTCCCG GAGACGGTCA	CGCGAATTAC GCGGCGATGT CCCGCGCAGG CCTAGGACGG AGCGCGCAA GCCACTACTG CCACCTTTGG AGACTGTGTA CGTCGAGGGC CTCTGCCAGT
33901	CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TCAGCGGGTG TTGGCGGGTG GCCATGACCC AGTCACGTAG	GTGCAACAGA CATTCGCCTA CGGCCCTCTG CTGTTCCGGC AGTCCGCCAC AGCTCCGCCAC AACCGCCAC AGCCCCCGT CCGTACTGGG TCAGTGCATC

FIG. 10D

APPROVED	C. G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

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4001 CGATAGCGGA GTGTATACTG GCTTAACTAT GCGGCATCAG AGCAGATTGT ACTGAGAGTG CACCATATGC GGTGTGAAAT ACCGCACAGA TGCCTAAGGA
GCTATCGCCT CACATATGAC CGAATTGATA CGCCGTAGTC TCGTCTAACA TGACTCTCAC GTGGTATACG CCACACTTTA TGGCGTGTCT ACGCATTCCT

4101 GAAATACCG CATCAGGCGC TCTTCCGCTT CCTCGCTCAC TGACTCGCTG CGCTCGGTGCG TTCCGGCTGCG TCCAGCGGTA TCAGTCACT CAAGGCGGGT
CTTTTATGGC GTAGTCCGCG AGAAGCGGA GAAGCGAGTG ACTGAGCGAC GCGAGCCAGC AAGCCGACGC CGCTCGCCAT AGTCGAGTGA GTTTCGCGCA

4201 AATACGGTTA TCCACAGAAAT CAGGGGATAA CCGAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAGGCC AGAACCCTTA AAAAGGCCG GTTGTGCGG
TTATGCCAAT AGGTGTCTTA GTCCCTTAT GTCCCTTTC TTGTACACTC GTTTCGCTTTCG TCTTTCGCTTTCG TCTTTCGCTTTCG CAACGACCGC

4301 TTTTTCATA GGTCTCGCCC CCCTGACGAG CATCACAAA ATCGACGCTC AATCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAC CAGGCGTTTC
AAAAGGTAT CCGAGGCGGG GGGACTGCTC GTAGTGTITT TAGCTGGAG TTCAGTCTCC ACCGCTTGG GCTGTCTGA TATTCTATG GTCCGCAAG

4401 CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCTT GCCGCTTACC GGATACCTGT CCGCCTTCTT CCGCTGCGG AGCGTGGCG TTTCTCATAG
GGGACCTTC GAGGAGCAC GCGAGAGGAC AAGGCTGGGA CCGCGAATGG CCTATGGACA GCGGAAAGA GGAAGCCCT TCGCACCGCG AAAGATATC

4501 CTCACGCTGT AGGTATCTCA GTTCGGTGTG GTTCGGTTCG TCCAAGCTGG GCTGTGTGCA CGAACCCCCC GTTCAGCCCC ACCGTGCGC CTTATCCGGT
GAGTCCGACA TCCATAGAGT CAAGCCACAT CCAGCAAGCG AGGTTCGACC CGACACAGT GCTTGGGGG CAAGTGGGG TGGCGACCG GAATAGGCCA

4601 AACTATCGTC TTGAGTCCAA CCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC GAGGTATGTA GCGGTGCTA
TTGATAGCAG AACTCAGGT GGGCCATTCT GTGTGAATA GCGGTGACC TCGTGGTGA CCATTGTCTT AATGCTCTG CTCCATACAT CCGCCACGAT

4701 CAGAGTTCTT GAAGTGGTGG CCTAACATAC GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG
GTCTCAAGAA CTTCAACCAC GGATTGATG CAGTGTGATC TTCTGTGATC AAACCATAGA CCGGAGACGA CTTCCGTCAA TGGAGCCTT TTTCTCAACC

4801 TAGCTCTGA TCCGGCAAC AAACCACCGC TGTAGCGGT GTTTTTTTT TTTGCAAGCA GCAGATTACG CCGAGAAAAA AAGGATCTCA AGAAGATCCT
ATCGAGAACT AGGCGGTTTG TTTGGTGGG ACCATCGCCA CCAAAAAAAC AACGTTCTGT CGTCTAATGC GCGTCTTTT TTCCTAGAGT TCTTCTAGGA

4901 TTGATCTTTT CTACGGGGTC TGACGCTCAG TGAACGAAA ACTCACGTTA AGGATTTTG GTCATGAGAT TATCAAAAAA GATCTTCACC TAGATCCTTT
AACTAGAAA GATGCCCCAG ACTGCGAGTC ACCTTGCTTT TGAGTGCAAT TCCCTAAAC CAGTACTCTA ATAGTTTTT CTAGAAAGTG ATCTAGGAAA

5001 TAAATTAAA ATGAAGTTTT AAATCAATCT AAAGTATATA TGAGTAACT TGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT
ATTTAATTTT TACTTCAAAA TTTAGTTAGA TTTTATATAT ACTCATTTGA ACCAGACTGT CAATGGTTAC GAATTAGTCA CTCCGTGGAT AGAGTCGCTA

5101 CTGTCTATTT GGTTCATCCA TAGTTGCCG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG
GACAGATAA GCAAGTAGGT ATCAACGGAC TGAGGGGACG CACATCTATT GATGCTATGC CCTCCCGAAT GGTAGACCGG GGTACGACG TTTACTATGGC

FIG.- 10E

APPROVED	C.G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

[illegible]

5201	CGAGACCCAC GCTCTGGTG GCTCTATTAA AGTCTATTAA TCAGATAATT	GCTCACC GC CGAGTGG CG AACCAACG TTGTTGCG AACCAACG	CCG TCAGATT AGTCTAAAT TAAGTAGTTC CTTCGATCTC	ACCAGCCAGC TGGTCGGTCG GCCAGTAAAT GCCAGTTAAT CGGTCAATTA	CGGAAGGCGC GCCTTCCCGG TCAAACGCGT AGTTTGGCA TCAAACGCGT	GAGCGCAGAA CTCGCGTCTT TGCAACAACG ACGTTGTTGC TGCAACAACG	GTGGTCTGC CACCAGGACG GTAACGACGT GGCATCGTGC GTAACGACGT	AACTTTATCC TTGAAATAGG CCGTAGCACC GGCATCGTGC CCGTAGCACC	GCCTCATCC CGGAGGTAGG ACAGTGGGAG TGTCACGCTC ACAGTGGGAG
5301									
5401	GTGCTTTGGT CAGCAAACCA	ATGGCTTCAT TACCGAAGTA	TCAGCTCCGG AGTCGAGGCC	TCAGCTCCGG AGTCGAGGCC	TCAAAGGCGAG AGTTCGGCTC	CCCCATGTTG GGGTACAAC	TGCAAAAAAG ACGTTTTTTC	CGGTTAGCTC GCCAATCGAG	CTTCGGTCCCT GAAGCCAGGA
5501	CCGATCGTTG GGCTAGCAAC	TCAGAAGTAA AGTCTTCATT	GTTGGCCGCA CAACCGGCGT	GTGTTATCAC CACAAATAGTG	TCATGGTTAT AGTACCAATA	GGCAGCACTG CCGTCTGTAC	CATAATTCTC GTATTAAGAG	GCCATCCGTA CGGTAGGCAT	AGATGCTTTT TCTACGAAAA
5601	CTGTGACTGG GACACTGACC	TGAGTACTCA ACTCATGAGT	ACCAAGTCAT TGGTTCAGTA	TCTGAGAATA AGACTCTTAT	GTGTATGCGG CACATACGCC	CGACCGAGTT GCTGGCTCAA	GCTCTTGCCC CGAGAACGGG	CGGGATAATA GCCCTATTAT	CCGCGCCACA GGCGCGGTGT
5701	TAGCAGAACT ATCGTCTTGA	TTAAAAGTGC AATTTTCACG	TCATCATTTGG AGTAGTAACC	AAAACGTTCT TTTTTGCAAGA	TCGGGGCGAA AGCCCCGCTT	GATCTTACCG CTAGAAATGGC	CTGTTGAGAT GACAACTCTA	CCAGTTTCGAT GGTCAAGCTA	GTAAACCCACT CATTTGGGTGA
5801	CGTGCACCCA GCACGTGGGT	ACTGATCTTC TGACTAGAAG	AGCATCTTTT TCGTAGAAAA	ACTTTCACCA TGAAAGTGGT	GCCTTTCTGG CGCAAAAGACC	GTGAGCAAAA CACCTCGTTT	AAAAATGCCG TGCTCTCCG	AAAAAAGGGA TTTTTTCCCT	ATAAGGGCGA TATTCCCGCT
5901	CACGGAATG GTGCCTTTAC	TTGAATACTC AACTTATGAG	ATACTCTTCC TATGAGAAGG	TTTTTTCATA AAAAAGTTAT	TTATTGAAGC AATAACTTCG	ATTATATCAGG TAAATAGTCC	GTATTGTCT CAATAACAGA	TACATATTG GTACTCGCT	AATCTATTTA TTACATAAAT
6001	GA AAAAATAA CTTTTATTAT	CAAAATAGGG GTTTATCCCC	TTCCGGGCAC AAGGCGGTG	ATTTCCCCGA TAAAGGGGCT	AAAGTGCCAC TTTCACGGTG	CTGACGTCTA GACTGCAGAT	AGAAACCATT TCTTTGGTAA	CATTAAACCTA GTAAATTGGAT	TAAAAATAGG ATTTTATATCC
6101	CGTATCACGA GCATAGTGCT	GGCCCTTTTCG CCGGGAAAGC	TCTTCAA AGAAGTT						

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FIG. 10F

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APPROVED	O.G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

DATE: 06/05/2000

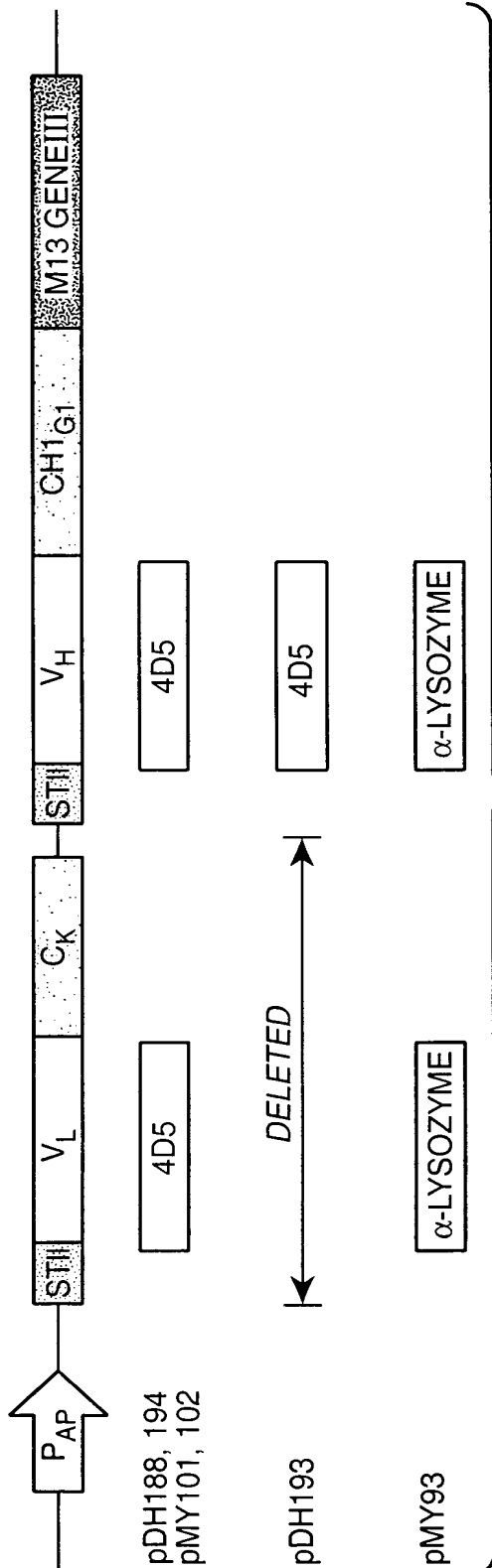


FIG. 11A

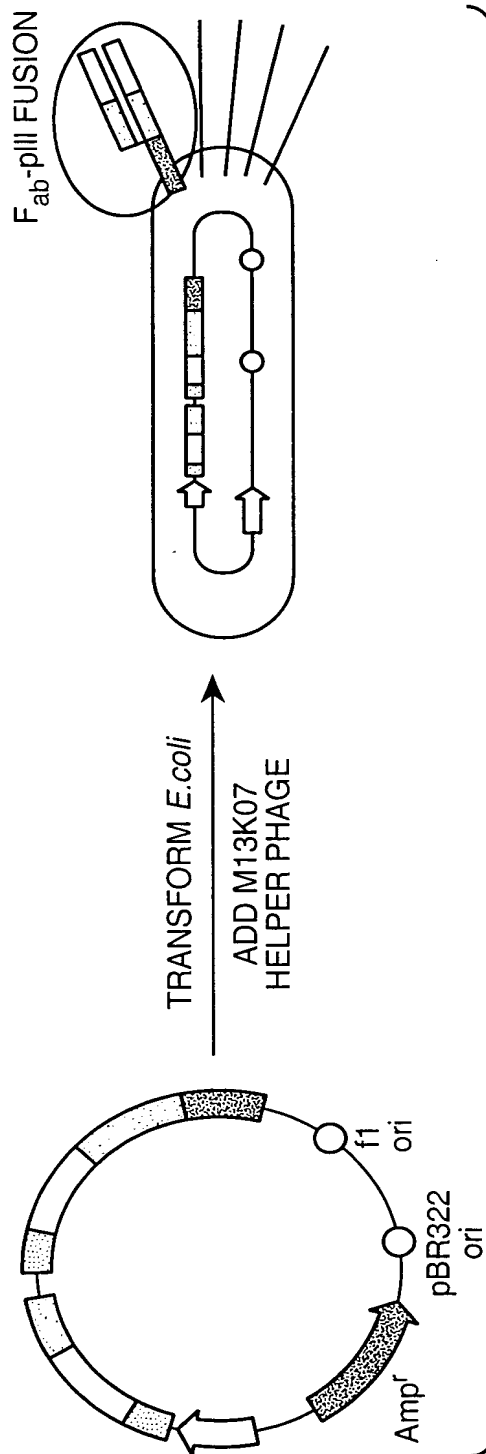


FIG. 11B

(E25) - LIGHT CHAIN

APPROVED BY DRAFTSMAN	DIQLTQSPSS	LSASVGDRVT	ITCRASQSVD	YDGDSYMNWY	QOKPGKAPKL	LIYAASYLES	GVPSRFSGSG
	SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF	IFPPSDEQLK	SGTASVVCLL
	NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDISTYLS	STLTLSKADY	EKKHVKYACEV	THQGLSSPVT
	KSFNRGEC						

(E25) - HEAVY CHAIN

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI
SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS	SASTKGPSVF	PLAPSSKSTS
GGTAALGCLV	KDYFPEPVT	SWNSGALTSG	VHTFPAVLQS	SGLYSLSSVV	TVPSSSLGTQ	TYICNVNHKP
SNTKVDKKVE	PKSCDKTHC	PPCPAPPELLG	GPSVFLFPPK	PKDTLMISRT	PEVTCVVVDV	SHEDPEVKFN
WYVDGVEVHN	AKTKPREEQY	NSTYRVVSVL	TVLHQDWLNG	KEYKCKVSNK	ALPAPIEKTI	SKAKGQPREP
QVYTLPPSRE	EMTKNQVSLT	CLVKGFYPSD	IAVEWESNGQ	PENNYKTTTP	VLDSDGSFFL	YSKLTVDKSR
WQQGNVFSCS	VMHEALHNHY	TQKSLSLSPG	K			

(E26) - LIGHT CHAIN

DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY	QOKPGKAPKL	LIYAASYLES	GVPSRFSGSG
SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF	IFPPSDEQLK	SGTASVVCLL
NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDISTYLS	STLTLSKADY	EKKHVKYACEV	THQGLSSPVT
KSFNRGEC						

(E26) - HEAVY CHAIN

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SITYDGSTNY	NPSVKGRITI
SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS	SASTKGPSVF	PLAPSSKSTS
GGTAALGCLV	KDYFPEPVT	SWNSGALTSG	VHTFPAVLQS	SGLYSLSSVV	TVPSSSLGTQ	TYICNVNHKP
SNTKVDKKVE	PKSCDKTHC	PPCPAPPELLG	GPSVFLFPPK	PKDTLMISRT	PEVTCVVVDV	SHEDPEVKFN
WYVDGVEVHN	AKTKPREEQY	NSTYRVVSVL	TVLHQDWLNG	KEYKCKVSNK	ALPAPIEKTI	SKAKGQPREP
QVYTLPPSRE	EMTKNQVSLT	CLVKGFYPSD	IAVEWESNGQ	PENNYKTTTP	VLDSDGSFFL	YSKLTVDKSR
WQQGNVFSCS	VMHEALHNHY	TQKSLSLSPG	K			

(E27) - LIGHT CHAIN

DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY	QOKPGKAPKL	LIYAASYLES	GVPSRFSGSG
SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF	IFPPSDEQLK	SGTASVVCLL
NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDISTYLS	STLTLSKADY	EKKHVKYACEV	THQGLSSPVT
KSFNRGEC						

(E27) - HEAVY CHAIN

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SIKYSGETKY	NPSVKGRITI
SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS	SASTKGPSVF	PLAPSSKSTS
GGTAALGCLV	KDYFPEPVT	SWNSGALTSG	VHTFPAVLQS	SGLYSLSSVV	TVPSSSLGTQ	TYICNVNHKP
SNTKVDKKVE	PKSCDKTHC	PPCPAPPELLG	GPSVFLFPPK	PKDTLMISRT	PEVTCVVVDV	SHEDPEVKFN
WYVDGVEVHN	AKTKPREEQY	NSTYRVVSVL	TVLHQDWLNG	KEYKCKVSNK	ALPAPIEKTI	SKAKGQPREP
QVYTLPPSRE	EMTKNQVSLT	CLVKGFYPSD	IAVEWESNGQ	PENNYKTTTP	VLDSDGSFFL	YSKLTVDKSR
WQQGNVFSCS	VMHEALHNHY	TQKSLSLSPG	K			

LIGHT CHAIN

E26

DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY	QQKPGKAPKL	LIYAASYLES
GVPSRFSGSG	SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF
IFPPSDEQLK	SGTASVVCLL	NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDSTYSL
STLTLSKADY	EKHKVYACEV	THQGLSSPVT	KSFNRGEC		

E27

DIQLTQSPSS	LSASVGDRVT	ITCRASKPVD	GEGDSYLNWY	QQKPGKAPKL	LIYAASYLES
GVPSRFSGSG	SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF
IFPPSDEQLK	SGTASVVCLL	NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDSTYSL
STLTLSKADY	EKHKVYACEV	THQGLSSPVT	KSFNRGEC		

HEAVY CHAIN

E26

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SITYDGSTNY
NPSVKGRITI	SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS
SASTKGPSVF	PLAPSSKSTS	GGTAALGCLV	KDYFPEPVT	SWNSGALTSG	VHTFPAVLQS
SGLYSLSSV	TVPSSSLGTQ	TYICNVNHKP	SNTKVDKKVE	PKSCDKTHT	

E27

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SIKYSGETKY
NPSVKGRITI	SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS
SASTKGPSVF	PLAPSSKSTS	GGTAALGCLV	KDYFPEPVT	SWNSGALTSG	VHTFPAVLQS
SGLYSLSSV	TVPSSSLGTQ	TYICNVNHKP	SNTKVDKKVE	PKSCDKTHT	

FIG._ 13

E26

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SITYDGSTNY
NPSVKGRITI	SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS
SEGGGSEGGG	SEGGGSDIQL	TQSPSSLSAS	VGDRVTITCR	ASKPVDGED	SYLNWYQQKP
GKAPKLLIYA	ASYLES	GVPS	RFSGSGSGTD	FTLTISLQ	EDFATYYCQQ
GTKVEIKR					SHEDPYTFGQ

E27

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SIKYSGETKY
NPSVKGRITI	SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGLVTVS
SEGGGSEGGG	SEGGGSDIQL	TQSPSSLSAS	VGDRVTITCR	ASKPVDGED	SYLNWYQQKP
GKAPKLLIYA	ASYLES	GVPS	RFSGSGSGTD	FTLTISLQ	EDFATYYCQQ
GTKVEIKR					SHEDPYTFGQ

FIG._ 14

APPROVED	Q.G. FIG.	CLASS	SUBCLASS
	BY		

LIGHT CHAIN

E26

DIQLTQSPSS	LSASVGDRV	ITCRASKPVD	GEGDSYLNWY	QQKPGKAPKL	LIYAASYLES
GVPSRFSGSG	SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF
IFPPSDEQLK	SGTASVVCLL	NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDSTYSLS
STLTLSKADY	EKHKVYACEV	THQGLSSPVT	KSFNRGEC		

E27

DIQLTQSPSS	LSASVGDRV	ITCRASKPVD	GEGDSYLNWY	QQKPGKAPKL	LIYAASYLES
GVPSRFSGSG	SGTDFTLTIS	SLQPEDFATY	YCQQSHEDPY	TFGQGTKVEI	KRTVAAPSVF
IFPPSDEQLK	SGTASVVCLL	NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKDSTYSLS
STLTLSKADY	EKHKVYACEV	THQGLSSPVT	KSFNRGEC		

HEAVY CHAIN

E26

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SITYDGSTNY
NPSVKGRITI	SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGTLLVTVS
SASTKGPSVF	PLAPSSKSTS	GGTAALGCLV	KDYFPEPVTV	SWNSGALTSG	VHTFPAVLQS
SGLYSLSSVV	TVPSSSLGTQ	TYICNVNHKP	SNTKVDKKVE	PKSCDKTHTC	PPC

E27

EVQLVESGGG	LVQPGGSLRL	SCAVSGYSIT	SGYSWNWIRQ	APGKGLEWVA	SIKYSGETKY
NPSVKGRITI	SRDDSKNTFY	LQMNSLRAED	TAVYYCARGS	HYFGHWHFAV	WGQGTLLVTVS
SASTKGPSVF	PLAPSSKSTS	GGTAALGCLV	KDYFPEPVTV	SWNSGALTSG	VHTFPAVLQS
SGLYSLSSVV	TVPSSSLGTQ	TYICNVNHKP	SNTKVDKKVE	PKSCDKTHTC	PPC

FIG._15